

Db 422 FGPDIRWEFGSTEGNVGLMNVYGHGAVGRTSCILRLMTPPELYQFDIETAEPLRDKQ 481
QY 413 YCVRPKGEVGLLVCKITQITLPNGYAGAKAOTEKKLRDVKPKGDLNFNSGDLMDVHE 472
Db 482 FCIPVPGKPGLLTKVRKNQPFGLYRGSGAESNRKLVANVRVGDLYFNTGDLVTLQDE 541
QY 473 NFYIFDRVGDTPFRKGNVAVTEADTVGLVDFVQEVNNVGVHVHPDHEGRIGMASIKMK 532
Db 542 GFFYQDRLGDTFRKGNVAVTEADTVGLVDFVQEVNNVGVHVHPDHEGRIGMASIKMK 601
QY 533 ENHEFGKLFQHIADYPSYARPRFRIQDTIETITGTFKHKMTLVVEGFNPVAVIKDAL 592
Db 602 PGKTFDQKLYQHVRSWLPAYATPHFIRIQDSLEITNTYKLVKSRLVREGPDVGIIADPL 661
QY 593 YFLDDTAKMVPMTEDIYNAISAKTLK 620
Db 662 YILDNAQOTFRSLMPDVPYQAVCEGTWKL 689

RESULT 2

A53093
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Sep-2000
C:Accession: A53093; 149132
R:Schaffer, J.E.; Lodish, H.F.
Cell 79, 427-436, 1994
A:Title: Expression cloning and characterization of a novel adipocyte long chain fatty acid
A:Reference number: A53093; MUID:95042740
A:Accession: A53093
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-646 <S>
A:Cross-references: GB:U15976; NID:9563828; PIDN:AACT1060.1; PID:9563829
C:Genetics:
A:Gene: FATP
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase homologous
F:124-604/Domain: acetate--CoA ligase homology <ACL>

Query Match 31.9%; Score 1044; DB 1; Length 646;
Best Local Similarity 40.0%; Pred. No. 7.6e-73;
Matches 247; Conservative 83; Mismatches 245; Indels 42; Gaps 11;
QY 33 FLKVAAGVRVRVSG-----QRRPARTILRAFLERAKOTPHKPFLLFRDETL 79
Db 43 FLRIVCKTARRDLGLSLVLRVLELRRHRRAGDTIPCFQAVARQPERALVDASSGI 102
QY 80 --TYAQVDRSNQVARELHDLGLRGDCVALLMGNEPAYVWLWGLVKLGCMACLNYN 137
Db 103 CWTFAQLDTSNAYAN-LFRQLGFAPGDVAVFLEGRPEFVGLWGLAKAGVVAALLNVN 161
QY 138 IRASLILHQCQCGAKVLLVSPLEQAVEILPSLKKDDVSIYVSRSTNDCIDSLDK 197
Db 162 LRREPLAFCLGTSNAKALITVGGMAAAVAEVSQLGK-----LLKFCSDGLGPESILPD 216
QY 198 VD-----EVSTPEI---PESRSEVTFSTPALYITSGTGLPKAAMTHQRIWYGTG 247
Db 217 TQLDPLMAEAPTTPLAQAPGKMDRLF-----YIYTSCTGLPKAAIIVHRYRRIA 271
QY 248 LTFVS-GLKADDVYIYLPYHSAALLIGHCIVAGATLAKTKSASQFDDCRKYNV 306
Db 272 FGHSHYSMAADVLYDCLPLYHSAAGNIMGVQCQVYGLTVVLRKFSASRFDWDCVKYN 331
QY 307 TVIYIGELLRYLNSPKQPNDRDHKVRALGNLGRDVMVRQVFRKFGDICIYEFYAATE 366
Db 332 TVVYIGELCYLLRQVPRVQEHVRVRLAVGNLRAPIWEEFTQRGVYQIGEFYATE 391
QY 367 GNIGFMNARKVAGVNVVYVQKLIYDLYKVDVEKDEPVRDENGVCYVRVPGVGLLV 426
Db 392 CNCSTIANMDGKVGCGFNSRLTHVYPIRLVKNEDTMEPLRDESEGLICPCQPEGLV 451
QY 427 CKITQLTP---FNGYAGAKAOTEKKLRDVKPKGDLVFNNSGDLMDVHDENFIYFHRVGD 483

Db 452 GOINQOPLRFREDGYVSDSA-TNKKTAHSVFRKSDSAYLSGDLVMDLGYMYFRDRSGD 510
QY 484 TFRWKGNAVTEADTVGLVDFVQEVNNVGVHVHPDHEGRIGMASIKMKENHEFDEKFLF 543
Db 511 TFRWGNVSTTEAVEAVLSRLGQTDVAVYGVAVPGVGVGKAGMAAI-ADPHSOLDPNSMY 569
QY 544 QHIADYLPSPARPRFRIQDTIETITGTFKHKMTLVVEGFNPVAVIKDALYFLDDTAKMYV 603
Db 570 QELQKVLASARPIFLKLLPOVDTTGTFKIQKRLQREGFDPRTSDRLEFLDKQGRYV 629
QY 604 PMTEIYNAISAKTLK 620
Db 630 PLDERVHARICAGDFSL 646

RESULT 3

T21498
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T21498
R:Baynes, C.
Submitted to the EMBL Data Library, April 1996
A:Reference number: Z19430
A:Accession: T21498
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-650 <WTL>
A:Cross-references: EMBL:Z70684; PIDN:CRA94602.1; GSPDB:GN00022; CESP:F28D1.9
A:Experimental source: Clone F28D1
C:Genetics:
A:Gene: CESP:F28D1.9
A:Map position: 4
A:Introns: 55/2; 87/2; 120/3; 187/1; 241/1; 356/1; 395/1; 600/1
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase homologous
F:123-609/Domain: acetate--CoA ligase homology <ACL>

Query Match 29.3%; Score 958; DB 2; Length 650;
Best Local Similarity 38.5%; Pred. No. 3.5e-66;
Matches 222; Conservative 97; Mismatches 225; Indels 32; Gaps 15;
QY 59 FLEKARQTHPKPFL--LFRDETLYAQVDRSNQVARELHDLGLRGDCVALLMGNEPA 116
Db 81 FLDIYVKNPNKPMIDTETNTTETAYEAFNAHCNRYANYFQG-LGYRSGDVVVALTWNSVE 139
QY 117 VVWLGLVGLKGCAMACLNIRAKSLHFCQCGAKVLLVSPELQ-----AAVEEILPSL 172
Db 140 FVAAMWGLAKGVVTAWLNSNLKREQLVHCITASKTRAITSVTLQNLMDLADQKL--F 197
QY 173 KDDVSIYVSRSTNDCIDSLDKVD--EVSTPEIPESRSEVTFSTPALYIYTSGTGL 231
Db 198 DVEGIEVSVGPKKNSGFKNLKKKLDQAITEP---KTLDIVDFKSLCFIYTSGTGM 254
QY 232 PKAAMITHOR---IHWGTGLTFVSLKADDVYIYLPYHSAALLIGHCIVAGATLAL 288
Db 255 PKAAVKKHFRYYSIYAVGAASKF--GIRSDRMVSMPIYHFAAGILGVQALLGGSCVI 312
QY 289 RTKFSASQFDDCRKYNVTVIYIGELLRYLNSPKQPNDRDHKVRALGNLGRDVMVRQ 348
Db 313 RKKFSASNFWRDVKVYDCTVSQYIGELCYLLAQPVVEESRHRMLVGNLRAEIWOP 372
QY 349 FVFRGDCIYEFYAATEGNIGFMNARKVAGV--RVNYLQKKLIYDLYKVDKDEP 406
Db 373 FVDRF--RVRIYIGELYSTEGTSLNVDHGVGACGFLPSLTKKMHVRLRLKVDVDTGEA 431
QY 407 VRDENGVCYVRVPGVGLLVCKITQTP---FNGYAGAKAOTEKKLRDVKPKGDLVFNNS 463
Db 432 ITSDGLCIACNPGSGAMVSTIRKNNLLOFEGYLN-KKETNKKIIRDFVAKGDSCLT 490
QY 464 GDLLMVDHNFYIFHRVGDTRFKWGNVAVTEADTVGLVDFVQEVNNVGVHVHPDHEGR 523

Db 491 GDLHWDRLGYVFKDRTGTRWKGENVSTTEVEALLHPITGLSDATVYGVVEVPQREGR 550
QY 524 IGWASIKMKENHEFDGKLFQH-----IADYLPYARPRFLRIODTIEITGFKHKKMTL 578
Db 551 VGNASVVRVVSHEED-ETOFVHRVGRGARLASSLTSYAIPQFMRICQDQVETGTFKLKVTNL 609
QY 579 VEEGFNPAVVKDALYFLDDTAKMYVPMTEDIYNAIS 614
Db 610 QRLGIMDAP-SDSIYIYNSERNRNFVFDNDLRCKVS 644

RESULT 4
H83284
Probable very-long-chain acyl-CoA synthetase PA2893 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83284
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: H83284
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-608 <STO>
A:Cross-references: GB:AE004715; GB:AE004091; NID:g9948977; PIDN:AAG06281.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2893
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

Query Match 29.1%; Score 953; DB 2; Length 608;
Best Local Similarity 38.1%; Pred. No. 7.9e-66;
Matches 222; Conservative 94; Mismatches 210; Indels 56; Gaps 14;

QY 60 LEK-ARQTPKPFLLFRDETLTYAQVDRRSNOVARALHDLGLRGDCVALLMGNEPAYV 118
Db 48 LERAARLYPDNPVLDGQRRIYSYALFNWANELARAFKAE-GVHGVSVAVALNRRVELL 106
QY 119 WLWGLVLKGCAMACLNINIRAKSLHLCFCQCGAKVLLVSPQLQAAVEEILPSLKDDVS 178
Db 107 ATLAALAKLGAICALVNTQRGKVLVSLNLVKPGHFVVGELREVFVEVRHEVLGNAGH 166
QY 179 IYVSRSTNTDGDIDSLDKVDESTEPIPEWSR-----EVTFTSPAL 221
Db 167 CWVD-----DLGDPGSPM--GWRNLMRLAOGQTSNLEDTGRVRLKDSCF 214
QY 222 YIYSGTTGLPKAAMITHQRIW---YG---TGLTFVSLKADDDVIYITLPLFYHSAALLI 274
Db 215 YIYSGTTGLPKASIMSHG-KIKAYGFGHSGL-----GLGRDDVLYTLPCYHNNAVTV 269
QY 275 GHGCIIVAGATLALTKESASFQWDDCRKYNVTYIYIGELLRYLCNSPQKPNDRHKVR 334
Db 270 CWSAALAGGAAMALRRKFSASGFWKDVQHYRATCFYIGELCYLLNQPCCAEERNSLT 329
QY 335 LALGNGLRGDWVRQVRFKFGDICIYFYAATGEGNIMYARKVAGVRNVLQKKIITY 394
Db 330 CMIGNGLRPSWAEPKQRFETQRTETFYASSEGNGFTNFVNTQV-----FSPATY 383
QY 395 DLIKYDVEKDEFPVRDENGVCYVRPKGEVGLLVCKITQLTPENGAGAKAOPEKKLRDVF 454
Db 384 ATVRVDLENDRPVRDAKGFMEKVGKGEVGLLISEISAKWPDGYTD-PAKSEAVILKDDVF 442
QY 455 KGDLYFNSGDLIM---VDHENFYFHDVRGDTFRWKGENVATTEVADTVGLVDFQVEVN 511
Db 443 KKGDAFWNTGDLMDIGFKHQFV---DRLGDTFRWKGENVSTTEVENALGAFDGVEDAV 499
QY 512 VYGVHPDHEGRIGMASFKKENHEFDGKLFQHIADYLPYARPRFLRIODTIEITGTF 571
Db 500 VYGVHPDHEGRIGMASFKKENHEFDGKLFQHIADYLPYARPRFLRIODTIEITGTF 559

QY 572 KHRKMTLVVEGFNPAVVKDALYFLDDTAKMYVPMTEDIYNAI 613
Db 560 KYKKTDLKRDYDPAVSDKLFVRLPGSAGYQPLDAELYQAL 601

RESULT 5
D70609
Probable fadD6 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000
C:Accession: D70609
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Nature 393, 537-544, 1998
A:Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua
; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: D70609
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-597 <COL>
A:Cross-references: GB:293777; GB:AL123456; NID:g3261726; PIDN:CAB07829.1; PID:g19290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: fadD6
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase
F;93-555/Domain: acetate--CoA ligase homology <ACL>

Query Match 28.9%; Score 944; DB 2; Length 597;
Best Local Similarity 39.1%; Pred. No. 3.8e-65;
Matches 217; Conservative 92; Mismatches 210; Indels 36; Gaps 10;

QY 59 FLEKARQTPKPFLLFRDETLTYAQVDRRSNOVARALHDLGLRGDCVALLMGNEPAYV 118
Db 53 FODRAARYGRVFLKFGDQQLTYRDANATANYAAVLAAR-GVGPQGVGVIMLRNPSFTV 111
QY 119 WLWGLVLKGCAMACLNINIRAKSLHLCFCQCGAKVLLVSPQLQAAVEEILPS---LKKD 175
Db 112 LAMLATVKCGAIAAGMLNYHQGEVLAHSLGLLDKAVLIAESDLVSAVAECGSRGRVAGD 171
QY 176 DVSIIYVSRTSNTDGDIDSLDKVDESTEPIPEWSRSEVTFSTPALYIYTSGTGTPKAA 235
Db 172 VLVTVEDVERFATT-----APATNP---ASASAVQAKDTAFYIFTSGTGFPPKAS 217
QY 236 MITHQR-----IWTGTGLTFVSLKADDDVIYITLPLFYHSAALLIGHGCIIVAGATLALR 289
Db 218 VMTHHRWLRLALAVFGGNGLR---LKGSDTYLSCLPLYHNNALTAVSSVINSGLATLALG 273
QY 290 TKFSASFQWDDCRKYNVTYIYIGELLRYLCNSPQKPNDRHKVRALAGNLGDFVWRQF 349
Db 274 KFSASFQWDEVANRATAPFYIGEICRYLLNQPAKPTDRAHQVRVYICNGLRPEIWDER 333
QY 350 VKRFGDICIYFYAATGEGNIMYARKVAGVRNVLQKKIITYDOLIKYDVEKDEPVRD 409
Db 334 TTRFGVARVCEFYAASEGNSAFIN---IFNPRTAGVSPMPLAF--VEYDLDITGDLPLRD 387
QY 410 ENGICYVRPKGEVGLLVCKITQLTPENGAGAKAOPEKKLRDVKKGLDYFNSGDLMLV 469
Db 388 ASGRVRVPDGPGLLSRVNRLQPDGYTDPA-SEKLVARNAPRQDCWNTGDVMSF 446
QY 470 DHENFYFHDVRGDTFRWKGENVATTEVADTVGLVDFQVEVNYGVHVPDHEGRIGMASI 529
Db 447 QGMGHAFAVDRLDGTFRWKGENVATTEVADTVGLVDFQVEVNYGVHVPDHEGRIGMASI 506
QY 530 KMKENHEFDGKLFQHIADYLPYARPRFLRIODTIEITGTEKKHKKMTLVVEGFNPAV 589
Db 507 TLRAGAEFGQALARYVYGLPLGVALPVRVVGSLAHTTTFKSRKVELRNQAYG-ADIE 565
QY 590 DALYFLDDTAKMYVP 604
||| | | |

Db 566 DPLYVLGPDEGYVP 580

RESULT 6

T15879

hypothetical protein D1009.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000

C:Accession: T15879

R:Favella, T.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid D1009.

A:Reference number: Z18422

A:Accession: T15879

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-655 <FAV>

A:Cross-references: EMBL:U40938; NID:g1072169; PID:g1072173; PIDN:AAA81698.1; CESP:D1009

C:Gene: CESP:D1009.1

A:Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3; 569/3; 602/1

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

F:128-611/Domain: acetate--CoA ligase homology <ACL>

Query Match 28.6%; Score 936; DB 2; Length 655;
Best Local Similarity 36.9%; Pred. No. 1.8e-64;
Matches 244; Conservative 95; Mismatches 245; Indels 78; Gaps 19;

QY 6 YTVLAGLLFLPLVNLCCPYF-FQDIGYFLKVAAGRRVRS-YGQRRPA-----52

Db 10 FALVTFFVAVLVYNSVFWKVFYIGY-----VFRLLRTDFGRALATLPDRFAGLKL 64

QY 53 -----RTILRAFLKARQTPHKPFLFRD--ETLTVAQVDRRSNOVARAL 95

Db 65 LISVKSTIRGLFKKDRPIHEIFLNQVQHPNKVAIIIESGRQIYQELNALANQYAN-L 123

QY 96 HDHLGRQDCVALLMGNEPAYVWLGLVGLGCAMACLNINRAKSLHLHCCGCAKVL 155

Db 124 YVSEGYKMGDVALEFMSIDFPAIWLGLSKIGVSAFINSNKLPLELAHSINVSKCKSC 183

QY 156 LVS-----PELQAAVEELPSLKKDDVSIYVSVTSNTDG-----JDSFLDKVDVSTEP 205

Db 184 ITINILNLPFKAAREK---NLISDEIHLVFLAG--TQVDRHRSLOQDLHLFSEDE---PP 235

QY 206 IPESWRSEVFTSPALYITSTGTLPKAAMITHQR-IWYGTGLTFVSLGKADDDVIYTL 264

Db 236 VIDG----LNFERSVLCYIYSTGTTGNPKPAVIKHERFYFWLGMAGAKAFGINKSDVYITM 291

QY 265 PFYHSAALLIGHCIVAGATLALRTKFSASQFWDCCRYNVTIYQIGELLRYLCNSPQ 324

Db 292 PMYHSAAGIMGIGSLAFSTAVIRKFSASNFKDCVKYNVTATQYIGEICRYLLAANP 351

QY 325 KPNDRHKVRILALGNLGRDVRQFVKRFGDICIYEFYAATEGNIGFMNRYARKVGAVGRV 384

Db 352 CPEKQHNVRMLMGNLGRGQIWEFVCRGKIKIGELYSTEGNSINVINVDNHVGCAGFM 411

QY 385 NYLQK--KIITYDLIKYDVEKDEPVRDENGVCYVRPKGEVGLLYCKITQ---LTPNGYA 439

Db 412 PIYPHIGSLPYRLIKVDRTAGELEKDKGLCPVPGTGEVGVYKEKIDILLKEGYV 471

QY 440 GAKAOTEKKLRLRVFKGDLFYNSGDLVDHNFYIFHDRVGDTPFRWGENVAITEVAD 499

Db 472 -SEGDTAKTIYRVFKHGDVFASGDLHWDLLGYLYFVDRCGDTPFRWGENVSTTEVSG 530

QY 500 TVGLVDVQVBNVYGVHVPDHEGRIGMASIKMKENHEFGGKLFQIADY-----LPS 552

Db 531 ILQPMVDVEDATYGVTVGKMEGRAGMAGIVVK-----DGTDEKEFIADITSRLTENLAS 585

QY 553 YARPRFLRIQDTITGTGTFKHKMTLVEEGFNPAVTK-DALYFLDDTAKMYVPMTEDIYN 611

Db 586 YAIPIVFLRCKEVDRTGTGTFKLLKTDLQKQYDLVACKGDPYIYWSAAEKSYKPLTDKMQQ 645

QY 612 AI 613

Db 646 DI 647

RESULT 7

T43052

fatty acid transport protein - fungus (Cochliobolus heterostrophus)

C:Species: Cochliobolus heterostrophus, Bipolaris maydis

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000

C:Accession: T43052

R:Oeser, B.M.

FEMS Microbiol. Lett. 165, 273-280, 1998

A:Title: PKC1, encoding a protein kinase C, and FAT1, encoding a fatty acid transport

A:Reference number: 222303; MUID:98415124

A:Accession: T43052

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-643 <OES>

A:Cross-references: EMBL:Y15839; NID:g2687848; PIDN:CAA75802.1; PID:g2687850

A:Experimental source: strain C2 (ATCC 48329)

C:Genetics:

A:Gene: fat1

A:Introns: 169/3; 478/2

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

F:121-599/Domain: acetate--CoA ligase homology <ACL>

Query Match 27.9%; Score 913.5; DB 2; Length 643;
Best Local Similarity 34.9%; Pred. No. 9.8e-63;
Matches 210; Conservative 112; Mismatches 238; Indels 41; Gaps 12;

QY 39 VGRVRSYVGRRPARTIL--RAFLEKARQTPHKPFLFRDETLYAQVDRRSNOVARALH 96

Db 65 INRRV---AOKR---VLTHHIFQEQVQKOSNHPFLIFEKGTWSYKEFSAYTRVANNLI 117

QY 97 DHLGLRGDCVALLMGNEPAYVWLGLVGLGCAMACLNINRAKSLHLHCCGCAKVL 156

Db 118 DELDVQGVEMVADGGSAEHLMLWALDAIGAATSLNWLNTGAGLHCKICECFVI 177

QY 157 VSPLEQAAVEELPSLKKDDVSIYVSVTSNTDGIDSLDKVDVSTEPPEPESWRSEVTF 216

Db 178 ADIDIKANIEPCGELEETGINIHVD-----PSFISSLN--NNTPIDSRSTENIEL 227

QY 217 STPALYITSTGTLPKAAMI-THQRWYGTGLTFVSLGKADDDVIYTLFYHSAALLIG 275

Db 228 DSVRGLIYTSGTLGPKGVFISTGRELRTDWSISKYLNLPKPTDRMYTCMPLYHAAHSLC 287

QY 276 IHGCIIVAGATLALRTKFSASQFWDCCRYNVTIYQIGELLRYLCNSPQPNDRDHKVR 335

Db 288 TASVTHGGGTVVLRSKTSKSHKFWPEVVAEANILOYVELGRYLLNGPKSPYDRAHKVQM 347

QY 336 ALGNLGRDVMRQVRKFGDICIYEFYAATEGNIGFM-----NYARKVGAVGRVN 385

Db 348 AWGNMRPDVWEAFREERNIPITHELVAATDG-LGSMTNRRNAGPFTANCIALRGLIHWK 406

QY 386 YLQKIIITDYDLIKYDVEKDEPVRDENGVCYVRPKGEVGLLYCKIT--QLPFGNGYAGAKA 443

Db 407 FRNOEV-----LVKMDLDTDEIMDRNGFAIRCAVNEPQMLFRTPETLAGAPSYNNET 462

QY 444 QTEKKLRDVKFGDLFYNSGDLHWDHNFYIFHDRVGDTPFRWGENVAITEVADTVGL 503

Db 463 ATQSRITDVFQKGLWPKSGDMLRQDAEGRVYFVDRIGDTFRWKSENVSTNEVADVAGT 522

QY 504 VDFQVQVNVYGVHVPDHEGRIGMASIKMKENHEFGGK--KLQFIADYLYPSYAPRELRI 561

Db 523 FPQIAETNVYGLVPGNDGRVRSNCHGRRRDRVDIRFAALAKHARDRLPGYAVPLELRV 582

QY 562 QDTTEITGTFKHKMTLVEEGFNPAVI--KDALYFLDDTAKMYVPMTEDIYNALSATLK 619

Db 583 TPALYETGTLKIQGRUKQEGIDPKTSGEDKLYLWPPGSDIYLPFGKMEQGVIVDRIR 642

QY 620 L 620

Db 643 L 643

RESULT 8

S45899

probable membrane protein YBR041w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YBR041

C;Species: Saccharomyces cerevisiae

C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000

C;Accession: S45899

R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.

submitted to the Protein Sequence Database, August 1994

A;Reference number: S45899

A;Accession: S45899

A;Molecule type: DNA

A;Residues: 1-623 <AND>

A;Cross-references: EMBL:Z35910; NID:g536263; PIDN:CAA84983.1; PID:g536264; MIPS:YBR041w

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:PAT1

A;Cross-references: SGD:S0000245; MIPS:YBR041w

A;Map position: 2R

C;Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase bc

C;Keywords: transmembrane protein

F;1-27/Domain: transmembrane #status predicted <TM1>

F;55-71/Domain: transmembrane #status predicted <TM2>

F;133-623/Domain: acetate--CoA ligase homology <ACL>

F;149-167/Domain: transmembrane #status predicted <TM3>

F;304-322/Domain: transmembrane #status predicted <TM4>

Query Match

Best Local Similarity 22.8%; Score 744.5; DB 2; Length 623;

Matches 191; Conservative 96; Mismatches 236; Indels 59; Gaps 16;

QY 24 PYFFDIDGVLKVAAGR-----RVSYGQRPARPILRAFLKARQTPHPKPF 72

Db 58 PYFLKSV--FCYIIDRRHRRFQNWYLFKQVQGDHL-AISYTRPMAEKE----- 106

QY 73 LPRDETLTAQVDRRSNOVARALHDHGLRGDCVALLMGNEPAYVWLGLVKLG 132

Db 107 -PQLEFFYIETYNVLKSLHLLHFDYVQAGDYVAIDCTNKLPLFVLWLSWLNIGATPA 165

QY 133 CLNYNIRAKSLHLCQCCGAKVLLSPQLAAVEILPSLKK--DDVSIYVSVTSNTDG 190

Db 166 FLNNTKGTPLVHLSKISNITQVFDPPASNPIRESEEEIKNALPDVKNLYLEQ----- 220

QY 191 IDSFLDKVDVSTPIPESEWSE-----VTFSTPALYIYTSOTGLPKAAMTHORIW 243

Db 221 -----DLMHLLNSQSPFLOQDNVTRPLGLTDFKPSMLIYTSOTGLPKSAIMSWRKSS 275

QY 244 YGTGL-TEVSGLKADDVYITLPFVHSAALLIGHGICVAGATLALRTKFSASQFWD 302

Db 276 VGCQVEGHVLMHNTSVFTAMPLFHSSTAALLGACAILSHGCGLALSHKFSASTFWQVY 335

QY 303 KYNVTIYQIGELLYLNCSPQNDPNDHVKVRLALGNLGRDGVWQVFRFGDICIYEFY 362

Db 336 LTGATHIYQVGEVCRYLLHTPISRYEKMHKVKVAYGNGLRPDIWODFRKRNIEVIGEFY 395

QY 363 AATEGNIGFMNAR---KVGAVGRVNYLOKKIITYD--LKYDVEKDEPV-RDENGVCVR 416

Db 396 AATEAPATTTTQKDGFGIGACRNVTGIOMFLSFQOTLVRMDPNDDSVIYRNSKGCEV 455

QY 417 VPKGEVGLLVCKI----TQTFPFNGYAGAKQTEKKLRDVKFKGDLVYNSGDLMLVDHE 472

Db 456 APVGPGEMLRIFFPKKPTSFQYGLGNAKETSKVVRDVRFGDADWYRCGDLMLKADEY 515

QY 473 NFIFYHEDVGRFTFRKGENVATTEVAD--TVGLVDFVQENVYGVHVPDHEGRIGMASIK 530

Db 516 GLWFLDRMGDTFRKSENSTTEVEDQLTASNKEQYQAVLVGVGKVPKVEGRAGAVIK 575

QY 531 MKENH-EFDGK-KLFQHIAD--YLPVSARPRFLRIQDTIET 568

Db 576 LTDNSLDITAKTKLLNDSLSRLNLPSPYAMPFLFVKFVDEIKMT 617

RESULT 9

D70806

probable fadD17 protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000

C;Accession: D70806

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A;Reference number: A70500; MUID:98295987

A;Accession: D70806

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-502 <COL>

A;Cross-references: GB:AL123456; NID:g3261554; PIDN:CAA17743.1; PID:g292

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: fadD17

C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F;51-486/Domain: acetate--CoA ligase homology <ACL>

Query Match

Best Local Similarity 12.2%; Score 398.5; DB 2; Length 502;

Matches 149; Conservative 78; Mismatches 218; Indels 85; Gaps 20;

QY 74 FRDETLTAQVDRRSNOVARALHDHGLRGDCVALLMGNEPAYVWLGLVKLG 128

Db 25 FEDSFTSWDRHRIHGAIAAALRERLDPAPPHVGVLLQNTFFSATLVAGALSGIVPVG 84

QY 129 CAAACLYNIRAKSLHLCQCCGAKVLLV---SPELQAAVEEILPSLKKDDVSIYVSVTS 185

Db 85 -----LNPVRGAALAGADIAKADCOLVLTGSGSAEVPADVEHI----- 122

QY 186 SNTDGDIDSLDKVDVSTPIPESEWSEVTFSTPAL-----YIYTSOTGLPKAAMTHQ 240

Db 123 ----NVDSP-PEWTDVAAHR-----DTEVFRSADLADLFMLIFTSGTGDPRKAVKCSHR 172

QY 241 RIWY-GTGLTFVSGLKADDVYITLPFVHSAALLIGHGICVAGATLALRTKFSASQFWD 299

Db 173 KVAIAGVTITQRFSLGRDDVCYVSMPLFHSNVLGVMAVAAACQGSMAALRRKFSASQFLA 232

QY 300 DCRKYNVTIYQIGELLYLNCSPQNDPNDHVKVRLALGN-GLRGDGVWQVFRFGDICI 358

Db 233 DVERYGATYANVGVKPLSVLATPELPDADNPLRAVGNVGVPGDIDR-FGRREGCV-V 290

QY 359 YEFYAATEGNIGF-MNARVKVAVGRVNYLOKKIITYDILIKYDVEKDEPVDRDENGVCVRV 417

Db 291 MDGFGSTEGVAITRTDTPAGALGP-----LPGGIQIVDPDTEGP-----C 332

QY 418 PRGEVGLLVCKITQLTP--FNGYAGAKQTEKKLRDVKFKGDLVYNSGDLMLVDHENFI 475

Db 333 PTGVGVGLV---NTAGPGGFEYINDEAAEAERMAAGV-----YHSGDLYARDADGVA 382

QY 476 YFHDRVGDTRFRKGENVATTEVADTVGLVDFVQENVYGVHVPDHEGRIGMASIKMKENH 535

Db 383 YFAGRLGDMWRVDGENLGTAPTERVLMRYPDATVAVYVPPVDPVGVQDV-MAAVLAPGT 441

QY 536 EFDGKLFQHIADYLPYSAR---PRFLRIQDTIETITGTFFKHKMTLVBERG 582

Db 442 KFDADK-FRAFLTEQDPLGHKQWPSVRSVRSAGLPRMTTFKVIKRLSAGS 490

RESULT 10

S40558

probable carnitine--CoA ligase (EC 6.2.1.1) - Escherichia coli

Qy	80	TYAQVDRRSNOVARALHDHJLGLRQGDQVALLMGNEPAYVWMLJGLVKVLCGACMACLNYNIR	139
Db	44	SYLENDQEIINRTANLFT-LGIRKGDVALHLDNCPFEFICFWGLGAKIGAIMVPINARLL	102
Qy	140	AKSLLHCFOCCGAKVLLVSPELQAAVEEILPSLKKDDVSIYKVSRTS-----NTDGDISFL	195
Db	103	CEESAWILQNSQACLLVYSQAQFPMYQOI---QOEDATQLRHICLTDVALPADDGVSSFT	159
Qy	196	DKVDEVSTFIPESWSEVFTSPALYIYTSQGTGLPKAMTHORIWY-GRGLTFVSGL	254
Db	160	QLKNO--QPATICYAPPLSTDTEILEFTSGTSTRPKGVVITHNLRFAGYISAWOQAL	216
Qy	255	KADDIVITLPEYHSAALLIGIHGCTVAGATLALRTKFSQFWDCCRKNYVTVIYQICE	314
Db	217	RDDVYLTVMPAFHIDCQTAAMAAASAGATFVLVEKYSARAFWQOVQYRATVTECIPM	276
Qy	315	LLRYLCSNPKPNDRDHKVR-LALGNLGRDWWQRPVKRFGDICIYEFVAAATEGNIGPW-	372
Db	277	MIRTLMWQPSANDQOHLREVFMFYNLSSEQEDAPCERFG-VRLTLYSGMTETIVGIIG	335
Qy	373	---NYAKVGAVGRVNYLQKKIITYDLIKYDVDEKDFPVRDENGICYVRVPKGEVGLVCK-	428
Db	336	DRPGDKRWPSTGRVGC-----YEAS---IRDDHNR--PLPAGIEGICIKG	378

Db 492 NMAKVKVPSYLEIR 505

RESULT 12

B70501

hypothetical protein rv1683 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: B70501

R: Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A: Reference number: A70500; MUID: 98295987

A: Accession: B70501

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-999 <COL>

A: Cross-references: GB:Z98268; GB:AL123456; NID:93261839; PIDN: CAB10940.1; PID: e332852;

A: Experimental source: strain H37RV

C: Genetics:

A: Gene: RV1683

Query Match 11.8%; Score 387.5; DB 2; Length 999;
Best Local Similarity 25.18; Pred. No. 1e-21;
Matches 151; Conservative 91; Mismatches 273; Indels 87; Gaps 18;

QY 36 VAAVGRRVRSYQGR-----RPAR-----TIIRAFLEKARQTPHPFLFRDETL 79

Db 415 VYAAANSRVTLAVERTLPLRLARLGQNDHTRISLGRIDEQAHPKFEFLFDGRVH 474

QY 80 TYAQVDRSNOVARALHDLGRODCVALLMGNEPAYVWLGLVKLGCMACLNINIR 139

Db 475 TYEAVNRINNVVRL-TAVGROGROGVLMETRPALVAIAALSRLGAV----- 524

QY 140 AKSLHCFQCCGAKVLLVSPLOAAVE-----EILPSLKKDDVSIVVSRSTNTDIDS- 193

Db 525 -----AVVMPDUTLSASVRLGRVTEILTPTNLDAARQLPGQVVLGGESR 572

QY 194 -----FLDKVDEVSTPIPSRWSEVTFPPALYITSGTGLPKAMIT 238

Db 573 DLDLPADALEOGQVIDMEKIDPDAVE-LPAMYRPNPGIARDLAFIAFSSADGLVAKQIT 631

QY 239 HORIW-----YGTGLTFVSGLKADDDVITLPPFVHSAALLIGIHGCIIVAGATLALTKFSA 294

Db 632 NYR-WAVSAFCTASTAALGRR--DTVYCLTPLHHESALLVSLGAVVGGTRIALSRLRP 688

QY 295 SQFWDCKRYVWTVIYIGELLRYLCSPOKPNDRDHKVRALGNGLRGDMVRQFVKRF 354

Db 689 DRFAEVRQYGVTVVSYTWAMLRDQVDDPAFVLHGNHPVRLFTGSGMPTGLWERYVEAFA 748

QY 355 DICIEYFAAPEGNIGFMNVA-RKVGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDNGY 413

Db 749 PAHVVEFATDGAQVLANVAGAKIGSKGRPLPGARV---ELGAYDAEDHLILENDRGF 805

QY 414 CVRPVKGEVLLVCKITQLTPFNFGYAGAKAOTEKKRLRDVFKKGLDYFNNSGDLMLMDHEN 473

Db 806 VQVAGVQVGVLLAQ--SRGPIDPTASVK-----RGVFAPADTWISTDYLFWRDDG 855

QY 474 FIYFHDRVGDFTFRMKGENVATTEVADTVGLVDFVQEVNRYGVHVPDHEGR-IGMASIKMK 532

Db 856 DWYLAGRGSVVRARGMVTEPTNALGLITGVDLAVTVGLV---RGRHVAVSAVTLL 912

QY 533 ENHEFDGKKLFQHIADYLPSPARPRFLRIODTTEITGTGFKHKWTLVEGFNPVAKAL 592

Db 913 PGATITADLAEVAS-MPVGLGPDIVHVPVQLTSLGTRPTVSALRANGI-PKAGROAW 970

QY 593 YF 594

Db 971 YF 972

RESULT 13

G70986

probable coA ligase - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000

C:Accession: G70986

R: Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A: Reference number: A70500; MUID: 98295987

A: Accession: G70986

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-532 <COL>

A: Cross-references: GB:Z95890; GB:AL123456; NID:93242245; PIDN: CAB09316.1; PID: g21310

A: Experimental source: strain H37RV

C: Genetics:

A: Gene: fadB1

C: Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F: 48-499/Domain: acetate--CoA ligase homology <ACL>

Query Match 11.8%; Score 385; DB 2; Length 532;
Best Local Similarity 26.8%; Pred. No. 6.8e-22;
Matches 142; Conservative 84; Mismatches 209; Indels 94; Gaps 21;

QY 107 VALLMGNEPAYVWLGLVKLGCMAC-LNYINIRAKSLHCFQCCGAKVLLVSPLOAAV 165

Db 55 IGSLLGNTPEML-AQLAAAGLGGVYVLCGLNTRRGDALAADVRADQCIWTVTDADHALL 113

QY 166 EELLPSLKKDDVSIVVSRSTNTDIDISFLDKYDVEVSTPIPSRWRS-----E 213

Db 114 -----DGLDLAGARILDST-----PRMAELVAGDGAFFPYRE 146

QY 214 VTFTPALYITSGTGLPKAMITH-QRIWYGTGLTFVSGLKADDDVITLPPFVHSAAL 272

Db 147 VDTMDPFMMIFTSGTSCNPKAVPVSHLMATFAGRSUTERFGLTEQDTCVSPFLHNAV 206

QY 273 LIGIHGCIIVAGATLALTKFSAQFWDCKRYVWTVIYIGELLRYLCSPOKPNDRDHK 332

Db 207 VAGWAPVWVSCAATAPAT-FSATGFLDDVRYHATYNYVKGFLAYILATPDRDDADNP 265

QY 333 VRLALGNGLRGDMVRQFVKRFQDICIYEFYAATE-----GNIGFMNYARKVG 379

Db 266 LRVAFGNEANDKDIEEFSSREFG-VQVEDGFGSTENAVIVIREPGTPPGSIG-----RG 317

QY 380 AVGRVNYLQKKIITYDLIKYDVEKDEPVRDNGYCVRVKGEVGLLVCKITQLTPFNFGYA 439

Db 318 AHGVYNGTETVTECAVAREDAHGALTNADE-----AIGELV-NTTSGSFGFTGY 366

QY 440 G-AKAQTEKKKLRDVKFKKGLDYFNNSGDLMLMDHENFIYFHDVRGDTFRWKGENVATTEVA 498

Db 367 NDPEANER-----MRHGMYW-SGDLAYRDSGWIYLAGRTADMVRVDGENLTAAPIE 418

QY 499 DTGVLDFVQEVNRYGVHVPD-HEGRIGMASIKMKENHEFDGKKLFQHIADYLP---SYA 554

Db 419 RILLRYKAINRVAVYA--VPDEYVGVQVMAALVLRAGDTFD-PDAFEAFDLAQPDLSKA 475

QY 555 RPRFLRIQDTFIETGTGFKHKWTLVEGFNPVAVIK-DALYFLDDDTAKWY 602

Db 476 RPRIRIADLPSTATHKVLKROLIDEG--TAVGKADTLWVREPRGSAY 522

RESULT 14

A69831

probable acid--CoA ligase (EC 6.2.1.-) yhfL [similarity] - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: A69831

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chedid, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, I.; Scanlon, A.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033

A:Accession: A69831

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-513 <KUN>

A:Cross-references: GB:290109; GB:AL009126; NID:g2633260; PIDN:CABL2867.1; PID:g2633363

A:Experimental source: strain 168

A:Genetics:

C:Gene: yhfL

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

C:Keywords: acid-thiol ligase

F:47-507/Domain: acetate--CoA ligase homology <ACL>

Query Match 10.8%; Score 354.5; DB 2; Length 513;
 Best Local Similarity 23.6%; Pred. No. 1.5e-19;
 Matches 127; Conservative 95; Mismatches 256; Indels 61; Gaps 15;

QY 61 EKARQPHKPFLLFRDITLYAQVDRSNQVARALHDHGLRGQDCVALLMGNEPAYVWL 120

Db 9 ETASEKPDSTACRQDHMTTYQLKQYQFADGLQE-AGMEKGDHLLALLGNSPDFFITA 67

QY 121 WLGLVKLGCCAMACINYNIRAKSLHLCFQCCGAKVLLVSPLOAARVEILPSSKKDDVSYT 180

Db 68 FFGALKAGIVVVPINPLYTTEIGYMLTNGDVKAIVGVSQLLPLXESMSHSLPKVELVL 127

QY 181 YVSTSTNDGID-----SFLDKVDEVT-----EPIPEWRSEVTSTPALYITSG 227

Db 128 CQTGEARPEADPEVRMKMTTFKILRPTSAKQONQEPVDD-----TAVILYITSG 178

QY 228 TTGLPKAMITHORIWYGTG-LTFVSGLKADDDVYITLPPYHSAALLIGHGICVAGATL 286

Db 179 TTGPKAMITHQNLVSNANDVAGYLGMDERDNNVCALPCHVFCLTVCMNAPLMSGAIV 238

QY 287 ALRTKFSASQFDDCRKYNVTYQYIGELLYLNCSPQKPNDRDHKVRALGNLGRDVG- 345

Db 239 LIEPQFSPASVFKLVKQOQATIEAGVPTMYNLFQHNHNGKDDFSSIRLCISGGSMPVA 298

QY 346 -WROFVKRFQDICIYEFAATEG-IGFMNARKVAGV-RVNYLQKKIITYDLIKY 399

Db 299 LLTAFEKFG-VTLEIGYGLSEASPVTCFNPFDGRKPPGSGISILHVENKVV----- 350

QY 400 DVEKDEPVRDENGVCVRPKGEVLCKITQTLTPFNGYAGAKAQTEKKLRDVFKKGDL 459

Db 351 -----DPLGRE-----LPAHQVGLVKGPNV-MKGYKMPMETE-----HALKDGWL 392

QY 460 YFNSGDLMLMDHNFITFHDVRGDTFRKGENVATTEVADTVGLVDVQEVNVGVHVPD 519

Db 393 Y--TGDARRDEDGYFYIVRKKMDITVGGVNYPREVEVLYSHPDVKEAVIG--VPD 448

QY 520 HEGRIGMASIKMKENHEFDGKKLFOHLADYLPVYARPRFLRIQDTIEITGTFKHKMTL 578

Db 449 PQSEANVGVVPRSGVTEEDIMQHCCKHLAKYKRAATFELDDIPKNTATKMLREAL 507

RESULT 15
 DB2824

regulator of pathogenicity factors XF0287 [imported] - Xylella fastidiosa (strain 9a5
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Nov-2000

A:Reference number: A82515; MUID:20365717

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82824

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-569 <SIM>

A:Cross-references: GB:AE003883; GB:AE003849; NID:g9105115; PIDN:AAF83100.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

M.; Tshukho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

C:Gene: XF0287

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

F:72-554/Domain: acetate--CoA ligase homology <ACL>

Query Match 10.2%; Score 335; DB 2; Length 569;
 Best Local Similarity 24.4%; Pred. No. 5.6e-18;
 Matches 139; Conservative 92; Mismatches 243; Indels 96; Gaps 20;

QY 53 RTILRAFLEKARQPHKPFLLFRDITLYAQVDRSNQVARALHDHGLRGQDCVALLMG 112

Db 25 RTIADVFTSVIKYRHCPCPAYTNFGKLTLYGEVLLTKQFASVLLNVLKKGDRALMML 84

QY 113 NEPAVYVWLGLVKLGCCAMACINYNIRAKSLHLCFQCCGAKVLLVSPLOAARVEILP 172

Db 85 NCLQTPVATFGALCAGLVVNVNPLYTARELKHQVLDAGSVLVVMDNFTVQVILIA-- 142

QY 173 KKDDVSIYVSTSTNDGID-----SFLDKVDEVTPEIPE-----SWRSEVTF--S 217

Db 143 ---DTPIKQVITTELGLDLDLDFPKRSLNFAVKHKKLVPEYQLPSPRINFREALALGSKHS 199

QY 218 TPALYI-----YTSGTTGLPKAMITHQRI-----WVGTLTFVSGLKADDDV 259

Db 200 MPPIHASSDLAFLOQYGTGTGPKGAMLTNRNMVNVNMQVQVSMQVLSLKEG---ET 256

QY 260 IVITPLFYHSAAL-----LIGHGC--IVAGATIALRTKFSASQFDDCRKYNVTYQY 311

Db 257 VLTALPLHIFALTANSLVFMKIGCNHLISNPR-NMRT-----FVKELQVRFTVITG 309

QY 312 IGELLYLNCSPQKPNDRDHKVRALGNL-----RGDWRQFVKRFQDICIYEFAATE 366

Db 310 VNTFLNKLTLPFPDKLDFSSILKIALGGWVIQSRVABQKQV-----HVPILIEAYGUTE 365

QY 367 GN-----IGFMNARKVAGVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGVCVRPKGEV 422

Db 366 ASPEACINPLNLOEHNGSIG-----MPLPSTDVC-----IKDQTN--TALPIGEM 408

QY 423 GLLVCKITQTLTPFNGYAGAKAQTEKKLRDVKPGDLYFNSGDLMLMDHNFITFHDVRG 482

Db 409 GELCIKGPQV--MKGYWQRPETSE-----VLDADGWLHTGDIYVKMDQKQGLFYIIDRKK 460

QY 483 DTFRWKGENVATTEVADTVGLVDVQEVNVYGVHVPDHEGRIGMASIKMKENHEFDGKKL 542

Mon Jul 16 18:57:59 2001

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Page 9

Db 461 EIIIVSGFNVPKEIEEVIAIPGVAEVAAG--VPDEQSGEVVKVIVKKDPMLTAEV 518

QY 543 FQHTADYLPYARPRFLRIQDTIEITGTFK 572

Db 519 KAAATNLTRYKLPRIIEFRATLPKTDVGK 548

Search completed: July 16, 2001, 18:13:54
Job time: 155 sec

